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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/436,060	11/08/1999	James T Kealey	014/002C	6093

22869 7590 07/02/2004

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EXAMINER	
GIBBS, TERRA C	
ART UNIT	**PAPER NUMBER**
1635	

DATE MAILED: 07/02/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

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SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.
09/436,060	09/26/2001	Kealey et al.	014/002C

EXAMINER	
Terra C. Gibbs	
ART UNIT	PAPER NUMBER
1635	

Please find below a communication from the EXAMINER in charge of this application

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 C.F.R. §1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 C.F.R. §1.821-1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures. For example, see the sequence on pages 13 and 14. The sequence of the PstI fragment is provided in SEQ ID NO:1, on pages 13 and 14. The sequence on page 13, at nucleobase 21, reads "0". At the end of the sequence, on page 14, it is disclosed that # = "7" is A or T. It it is unclear what "0" is intended to be. Page 14 discloses that # = "7" is A or T, however, the CRF, at SEQ ID NO:1, lists nucleobase 21 as a "G". The sequence listed in the disclosure does not appear to be the same as that listed in the CRF.

APPLICANT IS GIVEN 30 days FROM THE DATE OF THIS LETTER WITHIN WHICH TO COMPLY WITH THE SEQUENCE RULES, 37 C.F.R. §§ 1.821-1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 C.F.R. § 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 C.F.R. § 1.136. In no case may an applicant extend the period for response beyond the six month statutory period. Direct the response to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the response.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Terra C. Gibbs whose telephone number is (571) 272-0758. The examiner can normally be reached on M-F 9:00-5:00.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, John L. LeGuyader can be reached on (571) 272-0760. The fax phone number for the organization where this application or proceeding is assigned is 703-872-9306.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Karen A. Lacourciere

KAREN A. LACOURCIERE, PH.D
PRIMARY EXAMINER

Application No.: 09/436,060

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☒ 7. Other: It appears that the sequences listed in the disclosure are not the same as the sequences listed in the CRF as set forth in 37 CFR 1.821-1.825.

Applicant Must Provide:

☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
PatentIn Software Program Support
Technical Assistance.....703-287-0200
To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

Collection pursuant to the Budapest Treaty and granted accession number ATCC 75926. A PstI fragment of the ~2.4 kb SauIIIA1-HindIII fragment of clone 28-1 also contains the hTR sequence. The sequence of the PstI fragment is provided in SEQ ID NO:1, below. The nucleotides of hTR are indicated above the sequence indicated by stars and numbered 1 to 451. The template region is underlined.

```
  1 CTGCAGAGGATAGAAAAAAG0CCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG
    GACGTCTCCTATCTTTTTTC7GGGAGACTATGGAGTTCAATCAAAGTGGAAATTTCTTCC
    -PST1-

 61 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG
    AGCCTTCATTTCTGCGTTTCGGAAAGGGCCTGCACGCCTTCCCGTTGCAGGAAGGAGTAC

121 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCAACCAGCCCGCCCGAGAGAGTGACTC
    CGGCCTTTACCTTGAAATTAAAGGGCAAGGGGGTTGGTCGGGCGGGCTCTCTCACTGAG

181 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT
    AGTGCTCTCGGCGCTCTCAGTCGAACCGGTTAGGCACGCCAGCCGCCGGCGAGGGAAATA

                             1       10        20        30
                             ***********************************
241 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC
    TTCGGCTGAGCGGGCCGTCGCGTGGCCCAACGCCTCCCACCCGGACCCTCCCCACCACCG

       40        50        60        70        80        90
    ************************************************************
301 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG
    GTAAAAAACAGATTGGGATTGACTCTTCCCGCATCCGCGGCACGAAAACGAGGGGCGCGC

      100       110       120       130       140       150
    ************************************************************
361 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT
    GACAAAAAGAGCGACTGAAAGTCGCCCGCCTTTTCGGAGCCGGACGGCGGAAGGTGGCAA

      160       170       180       190       200       210
    ************************************************************
421 CATTCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC
    GTAAGATCTCGTTTGTTTTTTACAGTCGACGACCGGGCAAGCGGGGAGGGCCCCTGGACG

                          HTR
      220       230       240       250       260       270
    ************************************************************
481 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC
    CCGCCCAGCGGACGGGTCGGGGGCTTGGGGCGGACCTCCGGCGCCAGCCGGGCCCCGAAG

      280       290       300       310       320       330
    ************************************************************
541 TCCGGAGGCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGG
    AGGCCTCCGTGGGTGACGGTGGCGCTTCTCAACCCGAGACAGTCGGCGCCCAGAGAGCCC

      340       350       360       370       380       390
    ************************************************************
601 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG
    CCGCTCCCGCTCCAAGTCCGGAAAGTCCGGCGTCCTTCTCCTTGCCTCGCTCAGGGGCGC

      400       410       420       430       440       450
    ********************************************************
661 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT
    GCGCCGCGCTAAGGGACTCGACACCCTGCACGTGGGTCCTGAGCCGAGTGTGTACGTCAA

721 CGCTTTCCTGTTGGTGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT
    GCGAAAGGACAACCACCCCCTTGCGGCTAGCACGCGTAGGCAGTGGGGAGCGGCCGTCA

781 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG
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841 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA
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901 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC
    CGGCAAGGACGCACCCAAGAGGGCAGAAGGCGAAAAACAACGGAAAATACCAACATAATG

961 AACTTAGTTCCTGCTCTGCAG  (SEQ ID NO:1)  (# = "7" IS A OR T)
    TTGAATCAAGGACGAGACGTC
                  -PST1-
```

C. Regions Of hTR Accessible In The Telomerase Ribonucleoprotein

Regions of hTR that are accessible in the native telomerase ribonucleoprotein have been identified. The regions were identified in two ways. The first way involved contacting samples containing human telomerase with a variety of DNA polynucleotides having sequences complementary to the sequence of hTR under hybridization conditions, contacting the telomerase with RNase H, which digests the RNA strand of an RNA-DNA hybrid, and determining whether hTR had been cleaved. Antisense oligonucleotides that supported hTR cleavage were complementary to nucleotides 137-166, 290-319 and 350-380 of hTR. See Table 1 and Fig. 1. Specific polynucleotides capable of supporting RNase H cleavage are described in more detail in the Example. The second way involved oligo-decoration. This method indicated that nucleotides 167-193 also are accessible. Regions of hTR accessible in the telomerase ribonucleoprotein comprise these areas. Other accessible areas of hTR can be identified by similar assays using antisense polynucleotides whose sequences are substantially complementary to a nucleotide sequence selected from hTR. The RNA component of telomerase of other mammals also contains accessible regions in the telomerase ribonucleoprotein.

Accessible regions of the RNA component of telomerase and their uses are also described in United States patent application NO. 5,846,723, filed December 20, 1996 ~~(Kim et al., "Methods for detecting the RNA component of telomerase," Geron docket no. 015)~~.

III. INHIBITORY POLYNUCLEOTIDES

A. General

This invention provides inhibitory polynucleotides directed against the RNA component of telomerase that inhibit telomerase activity. Inhibitory polynucleotides can inhibit telomerase activity in a number of ways. According to one mechanism, the polynucleotide prevents transcription of the telomerase RNA component

RAW SEQUENCE LISTING DATE: 04/23/2004
PATENT APPLICATION: US/09/436,060A TIME: 11:19:50

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Output Set: N:\CRF4\04232004\I436060A.raw

<110> APPLICANT: Geron Corporation
Kealy, James T.
Pruzan, Ronald
Weinrich, Scott L.
<120> TITLE OF INVENTION: Inhibitory Polynucleotides Directed Against the RNA Component of Telomerase
<130> FILE REFERENCE: 014/002C
<140> CURRENT APPLICATION NUMBER: 09/436,060A
<141> CURRENT FILING DATE: 1999-11-08
<150> PRIOR APPLICATION NUMBER: 08/770,564
<151> PRIOR FILING DATE: 1996-12-20
<160> NUMBER OF SEQ ID NOS: 16
<170> SOFTWARE: PatentIn version 3.1
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<211> LENGTH: 981
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 1

ENTERED

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